



Dkt. 0575/50659/JPW/BJA

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants : David Baltimore et al.  
Serial No. : 08/813,323 (CPA) Examiner: Minh-Tam Davis  
Filed : March 10, 1997 Group Art Unit: 1642  
For : TRUNCATED CRAFT1 INHIBITS CD40 SIGNALING

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March 31, 2003

TECH CENTER 1600/2900

APR 09 2003

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Honorable Commissioner for Patents and Trademarks  
Washington, D.C. 20231

Sir:

AMENDMENT IN RESPONSE TO DECEMBER 31, 2002 OFFICE ACTION

This Amendment is submitted in response to a December 31, 2002 Office Action issued in connection with the above-identified application. A response to the December 31, 2002 Office Action is due March 31, 2003. Accordingly, this Amendment is being timely filed.

Please amend the subject application as follows:

In the Sequence Listing

Please replace the Sequence Listing with the corrected Sequence Listing attached hereto as **Exhibit A**.

In the Brief Description of the Figures

Please amend the Brief Description of the Figures as follows:

**Figure 1.** Predicted amino acid sequences of mouse (M) (SEQ ID NO:1) and human (H) (SEQ ID NO:2) CRAF1. The full-length mouse sequence is shown and numbered. The human sequence has one more amino acid than that of the mouse (indicated with a dot), but all numbers here refer to the mouse sequence. Dashes indicate positions in the human sequence that are identical to those in the mouse. The C26 clone obtained from the yeast two-hybrid screen contained the COOH-terminal region of CRAF1 starting from the position marked with an arrow.

**Figures 2A-D.** Potential structural domains of CRAF1. (A) Diagrams of three TRAF family members. Percentages of amino acid identity between CRAF1 and either TRAF1 or TRAF2 are shown. The TRAF domain was defined in the COOH-terminal region of TRAF1 and TRAF2 (19) (residues 356 to 562 for CRAF1 (SEQ ID NO:6)) but can be subdivided into TRAF-N and TRAF-C subregions according to sequence homology with CRAF1 as well as by the mapping assaying shown in Fig. 3. For CRAF1 (SEQ ID NO:1), the number of amino acids between homologous regions is indicated. (B) Helical wheel representation of residues 287 to 342 of CRAF1 (SEQ ID NO:7). The wheel starts with the inner residue Ile<sup>287</sup> at position a and diminishes with the outer residue Asn<sup>342</sup> at position g; "+" and "-" denote change of amino acid residues. (C) Predicted Zn fingers corresponding to residues 110